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FACULTY OF ENGINEERING AND TECHNOLOGY

Department of Biotechnology

Motif, Profiles, Patterns

✓When aligning protein sequences it is often apparent that certain regions or specific amino acids, are more conserved than others.

✓Such conserved regions are often conserved because they encode a part of the protein that is functionally important.

✓The term *motif* is use to refer to a part of a protein sequence that is associated with a particular biological function.

✓For example a region of a protein that binds ATP is called an ATP binding *motif*.�

✓Since these regions are conserved, they may be recognisable by the presence of a particular sequence of amino acids called a *pattern*.

✓A pattern is thus a qualitative description of a motif in terms of amino acid sequence.

XYZ

✓The concept of a *profile* extends this concept, allowing a quantitative description of a motif, by assigning probabilities to the occurrence of a particular amino acid at each position of a motif.

✓Thus profiles can be used to describe very divergent motifs.

✓The presence of a particular motif within a protein sequence can be used to suggest functions for uncharacterised proteins.

✓A number of databases have been constructed that attempt to describe particular protein motifs in terms of patterns and profiles.

XYZ

✓Search for patterns or profiles that are indicative of particular functional motifs within a query protein.

✓Some examples of such databases include:

✓����������� PROSITE - a collection of patterns and profiles

✓����������� Pfam - A collection of Profiles generated using hidden Markov models

✓����������� PRINTS - provider of fingerprints (groups of aligned, un-weighted motifs)

✓����������� BLOCKS - a database of weighted profiles or blocks

XYZ

abc

XYZ

abc

XYZ

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XYZ

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XYZ

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XYZ

abc

XYZ

abc

MCQs

1. A
2. A
3. A
4. A
5. A
6. A
7. A
8. A
9. A
10. A